

# SEQUENCE LISTING

<110> Pettersson-Fernholm, Annika Margareta  
Tomassen, Johannes Petrus Maria

<120> Neisseria Lactoferrin Binding Protein

<130> B45106C1

<140> Not Yet Assigned

<141> 2003-12-12

<150> 09/485,760

<151> 2000-02-15

<150> PCT/EP98/05117

<151> 1998-08-10

<150> GB 9717423.9

<151> 1997-08-15

<150> GB 9805544.8

<151> 1998-02-05

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2277

<212> DNA

<213> Neisseria meningitidis strain BNCV

<220>

<221> CDS

<222> (100)...(2274)

<400> 1

tcctgatttt tgttaattca ctataaaaac gggttgatat tatctgtaca tattaatata 60  
atgataatta ttattaatca aataggagga aaagtaggg atg tgt aaa ccg aat 114

Met Cys Lys Pro Asn

1

5

tat ggc ggc att gtc ttg ttg ccc tta ctt ttg gca tct tgt atc ggc 162  
 Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu Ala Ser Cys Ile Gly  
                   10                  15                  20

ggc aat ttc ggc gtg cag cct gtt gtc gaa tca acg ccg acc gcg tac 210  
 Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser Thr Pro Thr Ala Tyr  
                   25                  30                  35

ccc gtc act ttc aag tct aag gac gtt ccc act ccg ccc cct gcc aaa 258  
 Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr Pro Pro Pro Ala Lys  
                   40                  45                  50

cct tct ata gaa atc acg ccg gtc aac cgg ccc gcc gtc ggt gcg gca 306  
 Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro Ala Val Gly Ala Ala  
                   55                  60                  65

atg cgg ctg cca agg cgg aat act gct ttt cat cgt gaa gat ggc acg 354  
 Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His Arg Glu Asp Gly Thr  
                   70                  75                  80                  85

gaa att cca aat agc aaa caa gca gaa gaa aag ctg tcg ttt caa gaa 402  
 Glu Ile Pro Asn Ser Lys Gln Ala Glu Glu Lys Leu Ser Phe Gln Glu  
                   90                  95                  100

ggt gat gtt ctg ttt tta tac ggt tca aaa gga aat aaa ctt caa caa 450  
 Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly Asn Lys Leu Gln Gln  
                   105                  110                  115

ctt aaa agc gaa att cat aaa cgt gat tcc gat gta gaa att agg aca 498  
 Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp Val Glu Ile Arg Thr  
                   120                  125                  130

tca gaa aag gaa aat aaa aaa tat gat tat aaa ttt gta gat gca ggt 546  
 Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys Phe Val Asp Ala Gly  
                   135                  140                  145

tat gta tat gta aag gga aaa gat gaa att aag tgg act tca gat tac 594  
 Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys Trp Thr Ser Asp Tyr  
                   150                  155                  160                  165

aag cag ttt tcc aac cgc tta ggt tat gac ggt ttt gta tat tat tcc 642

Lys	Gln	Phe	Ser	Asn	Arg	Leu	Gly	Tyr	Asp	Gly	Phe	Val	Tyr	Tyr	Ser		
				170					175						180		
gga	gaa	cgt	cct	tcc	caa	tct	tta	ccg	agt	gcg	gga	acg	gtg	gaa	tat	690	
Gly	Glu	Arg	Pro	Ser	Gln	Ser	Leu	Pro	Ser	Ala	Gly	Thr	Val	Glu	Tyr		
			185					190					195				
tct	ggt	aac	tgg	caa	tat	atg	acc	gat	gcc	aaa	cgt	cat	cga	gca	ggt	738	
Ser	Gly	Asn	Trp	Gln	Tyr	Met	Thr	Asp	Ala	Lys	Arg	His	Arg	Ala	Gly		
		200					205					210					
aag	gcg	gtt	ggc	att	gac	aat	ttg	ggt	tat	tac	aca	ttt	tat	ggt	aac	786	
Lys	Ala	Val	Gly	Ile	Asp	Asn	Leu	Gly	Tyr	Tyr	Thr	Phe	Tyr	Gly	Asn		
	215					220					225						
gat	gtt	ggt	gca	act	tct	tat	gcg	gct	aag	gat	gtc	gac	gaa	agg	gaa	834	
Asp	Val	Gly	Ala	Thr	Ser	Tyr	Ala	Ala	Lys	Asp	Val	Asp	Glu	Arg	Glu		
230					235				240					245			
aaa	cat	cct	gct	aaa	tat	acg	gta	gat	ttc	ggt	aac	aaa	acc	ctg	acg	882	
Lys	His	Pro	Ala	Lys	Tyr	Thr	Val	Asp	Phe	Gly	Asn	Lys	Thr	Leu	Thr		
			250					255					260				
ggc	gag	ctg	att	aaa	aac	caa	tat	gtc	aaa	ccc	agt	gag	aag	caa	aaa	930	
Gly	Glu	Leu	Ile	Lys	Asn	Gln	Tyr	Val	Lys	Pro	Ser	Glu	Lys	Gln	Lys		
		265					270						275				
ccg	ctg	acc	att	tac	aac	atc	act	gcc	gat	tta	aac	ggc	aac	cgc	ttt	978	
Pro	Leu	Thr	Ile	Tyr	Asn	Ile	Thr	Ala	Asp	Leu	Asn	Gly	Asn	Arg	Phe		
		280					285					290					
acc	ggc	agt	gcc	aag	gtc	aat	cct	gat	tta	gcg	aaa	agc	cat	gcc	aat	1026	
Thr	Gly	Ser	Ala	Lys	Val	Asn	Pro	Asp	Leu	Ala	Lys	Ser	His	Ala	Asn		
		295				300					305						
aag	gag	cat	ttg	ttt	ttc	cat	gcc	gat	gcc	gat	cag	cgg	ctt	gag	ggc	1074	
Lys	Glu	His	Leu	Phe	Phe	His	Ala	Asp	Ala	Asp	Gln	Arg	Leu	Glu	Gly		
310					315				320					325			
ggt	ttt	ttc	ggc	gat	aag	ggg	gaa	gag	ctt	gcc	gga	cgg	ttt	atc	agc	1122	
Gly	Phe	Phe	Gly	Asp	Lys	Gly	Glu	Glu	Leu	Ala	Gly	Arg	Phe	Ile	Ser		
			330						335					340			

aac gac aac agc gta ttc ggt gta ttc gca ggc aaa caa aat agc ccc	1170
Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly Lys Gln Asn Ser Pro	
345 350 355	
gtg ccg tct gga aaa cac acc aaa atc ttg gat tct ctg aaa att tcc	1218
Val Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile Ser	
360 365 370	
gtt gat gag gca agt ggt gaa aat ccc cga ccg ttt gcc att tct cct	1266
Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Ala Ile Ser Pro	
375 380 385	
atg ccc gat ttt ggt cat ccc gac aaa ctt ctt gtc gaa ggg cat gaa	1314
Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly His Glu	
390 395 400 405	
att cct ttg gtt agc caa gag aaa acc atc gag ctt gcc gac ggc agg	1362
Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly Arg	
410 415 420	
aaa atg acc gtc agt gct tgt tgc gac ttt ttg acc tat gtg aaa ctc	1410
Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys Leu	
425 430 435	
gga cgg ata aaa acc gaa cgc ccc gcc gcc aaa ccg aag gcg cag gac	1458
Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys Pro Lys Ala Gln Asp	
440 445 450	
gaa gag gat tcg gac att gat aat ggc gaa gaa agc gaa gac gaa atc	1506
Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu Ile	
455 460 465	
ggc gat gaa gaa gaa ggc acc gaa gat gca gcc gca gga gat gaa ggc	1554
Gly Asp Glu Glu Glu Gly Thr Glu Asp Ala Ala Ala Gly Asp Glu Gly	
470 475 480 485	
agc gaa gaa gac gaa gcc aca gaa aac gaa gac ggc gaa gaa gac gaa	1602
Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp Gly Glu Glu Asp Glu	
490 495 500	
gct gaa gaa cct gaa gaa gaa tcg tcg gca gaa ggc aac ggc agt tca	1650
Ala Glu Glu Pro Glu Glu Glu Ser Ser Ala Glu Gly Asn Gly Ser Ser	
505 510 515	

aac gcc atc ctg cct gtc ccg gaa gcc tct aaa ggc agg gat atc gac	1698
Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp	
520 525 530	
ctt ttc ctg aaa ggt atc cgc acg gca gaa acg aat att ccg caa act	1746
Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asn Ile Pro Gln Thr	
535 540 545	
gga gaa gca cgc tat acc ggc act tgg gaa gcg cgt atc ggc aaa ccc	1794
Gly Glu Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro	
550 555 560 565	
att caa tgg gac aat cat gcg gat aaa gaa gcg gca aaa gca gta ttt	1842
Ile Gln Trp Asp Asn His Ala Asp Lys Glu Ala Ala Lys Ala Val Phe	
570 575 580	
acc gtt gat ttc ggc aag aaa tcg att tcc gga acg ctg acg gag aaa	1890
Thr Val Asp Phe Gly Lys Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys	
585 590 595	
aac ggt gta gaa cct gct ttc cgt att gaa aac ggc gtg att gag ggc	1938
Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn Gly Val Ile Glu Gly	
600 605 610	
aac ggt ttc cat gcg aca gcg cgc act cgg gat gac ggc atc gac ctt	1986
Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp Asp Gly Ile Asp Leu	
615 620 625	
tcc ggg cag ggt tcg acc aaa ccg cag atc ttc aaa gct aat gat ctt	2034
Ser Gly Gln Gly Ser Thr Lys Pro Gln Ile Phe Lys Ala Asn Asp Leu	
630 635 640 645	
cgt gta gaa gga gga ttt tac ggc ccg aag gcg gag gaa ttg ggc ggt	2082
Arg Val Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly	
650 655 660	
att att ttc aat aat gat ggg aaa tct ctt ggt ata act gaa ggt act	2130
Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Gly Thr	
665 670 675	
gaa aat aaa gtt gaa gct gat gtt gat gtt gat gtt gat gtt gat gtt	2178
Glu Asn Lys Val Glu Ala Asp Val Asp Val Asp Val Asp Val Asp Val	

680	685	690	
gat gct gat gct gat gtt gaa cag tta aaa cct gaa gtt aaa ccc caa			2226
Asp Ala Asp Ala Asp Val Glu Gln Leu Lys Pro Glu Val Lys Pro Gln			
695	700	705	
ttc ggc gtg gta ttc ggt gcg aag aaa gat aat aaa gag gtg gaa aaa			2274
Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn Lys Glu Val Glu Lys			
710	715	720	725
tga			2277

<210> 2

<211> 725

<212> PRT

<213> Neisseria meningitidis strain BNCV

<400> 2

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu			
1	5	10	15
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser			
20	25	30	
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr			
35	40	45	
Pro Pro Pro Ala Lys Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro			
50	55	60	
Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His			
65	70	75	80
Arg Glu Asp Gly Thr Glu Ile Pro Asn Ser Lys Gln Ala Glu Glu Lys			
85	90	95	
Leu Ser Phe Gln Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly			
100	105	110	
Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp			
115	120	125	
Val Glu Ile Arg Thr Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys			
130	135	140	
Phe Val Asp Ala Gly Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys			
145	150	155	160
Trp Thr Ser Asp Tyr Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp Gly			
165	170	175	
Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala			
180	185	190	
Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys			

195	200	205
Arg His Arg Ala Gly Lys Ala Val Gly Ile Asp Asn Leu Gly Tyr Tyr		
210	215	220
Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser Tyr Ala Ala Lys Asp		
225	230	235
Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr Thr Val Asp Phe Gly		
245	250	255
Asn Lys Thr Leu Thr Gly Glu Leu Ile Lys Asn Gln Tyr Val Lys Pro		
260	265	270
Ser Glu Lys Gln Lys Pro Leu Thr Ile Tyr Asn Ile Thr Ala Asp Leu		
275	280	285
Asn Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Pro Asp Leu Ala		
290	295	300
Lys Ser His Ala Asn Lys Glu His Leu Phe Phe His Ala Asp Ala Asp		
305	310	315
Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala		
325	330	335
Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly		
340	345	350
Lys Gln Asn Ser Pro Val Pro Ser Gly Lys His Thr Lys Ile Leu Asp		
355	360	365
Ser Leu Lys Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro		
370	375	380
Phe Ala Ile Ser Pro Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu		
385	390	395
Val Glu Gly His Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu		
405	410	415
Leu Ala Asp Gly Arg Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu		
420	425	430
Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys		
435	440	445
Pro Lys Ala Gln Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu		
450	455	460
Ser Glu Asp Glu Ile Gly Asp Glu Glu Glu Gly Thr Glu Asp Ala Ala		
465	470	475
Ala Gly Asp Glu Gly Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp		
485	490	495
Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Glu Ser Ser Ala Glu		
500	505	510
Gly Asn Gly Ser Ser Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys		
515	520	525
Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr		
530	535	540

Asn	Ile	Pro	Gln	Thr	Gly	Glu	Ala	Arg	Tyr	Thr	Gly	Thr	Trp	Glu	Ala	
545					550					555					560	
Arg	Ile	Gly	Lys	Pro	Ile	Gln	Trp	Asp	Asn	His	Ala	Asp	Lys	Glu	Ala	
			565					570						575		
Ala	Lys	Ala	Val	Phe	Thr	Val	Asp	Phe	Gly	Lys	Lys	Ser	Ile	Ser	Gly	
		580						585					590			
Thr	Leu	Thr	Glu	Lys	Asn	Gly	Val	Glu	Pro	Ala	Phe	Arg	Ile	Glu	Asn	
	595					600						605				
Gly	Val	Ile	Glu	Gly	Asn	Gly	Phe	His	Ala	Thr	Ala	Arg	Thr	Arg	Asp	
610					615						620					
Asp	Gly	Ile	Asp	Leu	Ser	Gly	Gln	Gly	Ser	Thr	Lys	Pro	Gln	Ile	Phe	
625				630					635						640	
Lys	Ala	Asn	Asp	Leu	Arg	Val	Glu	Gly	Gly	Phe	Tyr	Gly	Pro	Lys	Ala	
			645					650						655		
Glu	Glu	Leu	Gly	Gly	Ile	Ile	Phe	Asn	Asn	Asp	Gly	Lys	Ser	Leu	Gly	
		660						665					670			
Ile	Thr	Glu	Gly	Thr	Glu	Asn	Lys	Val	Glu	Ala	Asp	Val	Asp	Val	Asp	
	675					680						685				
Val	Asp	Val	Asp	Val	Asp	Ala	Asp	Ala	Asp	Val	Glu	Gln	Leu	Lys	Pro	
	690					695				700						
Glu	Val	Lys	Pro	Gln	Phe	Gly	Val	Val	Phe	Gly	Ala	Lys	Lys	Asp	Asn	
705				710					715						720	
Lys	Glu	Val	Glu	Lys												
			725													

<210> 3

<211> 2169

<212> DNA

<213> Neisseria meningitidis strain M981

<220>

<221> CDS

<222> (1)...(2166)

<400> 3

atg	tgt	aaa	cgc	aat	tat	ggc	ggc	att	gtc	ttg	ttg	ccc	tta	ctt	ttg	48
Met	Cys	Lys	Pro	Asn	Tyr	Gly	Gly	Ile	Val	Leu	Leu	Pro	Leu	Leu	Leu	
1				5				10						15		

gca	tct	tgc	atc	ggc	ggc	aat	ttc	ggc	gtg	cag	cct	gtt	gtc	gaa	tca	96
Ala	Ser	Cys	Ile	Gly	Gly	Asn	Phe	Gly	Val	Gln	Pro	Val	Val	Glu	Ser	
			20					25						30		



acg ccg acc gcg tac ccc gtc act ttc aag tct aag gac gtt ccc act	144
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr	
35 40 45	
tcg ccc cct gcc ggg tct tcg gta gaa acc acg ccg gtc aac cag ccc	192
Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Gln Pro	
50 55 60	
gcc gtc ggt gcg gca atg cgg ctg ttg aga cgg aat act gct ttt cat	240
Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His	
65 70 75 80	
cgt gaa gat ggc acg gca att ccc gat agc aaa caa gca gaa gaa aag	288
Arg Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys	
85 90 95	
ctg tcg ttt aaa gaa ggt gat gtt ctg ttt tta tac ggt tca aaa gaa	336
Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Glu	
100 105 110	
aat aaa ctt caa caa ctt aaa agc gaa att cat aaa cgt aat cct gag	384
Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asn Pro Glu	
115 120 125	
gca agc att acc aca tcg gaa aat gaa aat aaa aaa tat aat tat cgg	432
Ala Ser Ile Thr Thr Ser Glu Asn Glu Asn Lys Lys Tyr Asn Tyr Arg	
130 135 140	
ttt gtc agt gcc ggt tat gtg ttt act aaa aac gga aaa gat gaa att	480
Phe Val Ser Ala Gly Tyr Val Phe Thr Lys Asn Gly Lys Asp Glu Ile	
145 150 155 160	
gag aaa aca tcg gat gaa aag cag ttt tct aat cgt tta ggc tat gac	528
Glu Lys Thr Ser Asp Glu Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp	
165 170 175	
ggt ttt gta tat tat ctc gga gaa cat cct tcc caa tct tta ccg agc	576
Gly Phe Val Tyr Tyr Leu Gly Glu His Pro Ser Gln Ser Leu Pro Ser	
180 185 190	
gcg gga acg gtg aaa tat tcc ggc aac tgg caa tat atg acc gat gcc	624
Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala	

195	200	205	
ata cgt cat cgg aga ggt aag ggg gtt tcc agt gtg gat ttg ggt tat			672
Ile Arg His Arg Arg Gly Lys Gly Val Ser Ser Val Asp Leu Gly Tyr			
210	215	220	
acc aca tat tat ggt aat gaa att ggg gca gct tct tat gag gct agg			720
Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Ala Ser Tyr Glu Ala Arg			
225	230	235	240
gat gcc gat ggc cgg gaa aaa cat cct gcc gaa tat acg gtt aat ttc			768
Asp Ala Asp Gly Arg Glu Lys His Pro Ala Glu Tyr Thr Val Asn Phe			
	245	250	255
gac aaa aaa aac ctg gaa ggt aag ttg att aaa aat cag tat gtg caa			816
Asp Lys Lys Asn Leu Glu Gly Lys Leu Ile Lys Asn Gln Tyr Val Gln			
	260	265	270
aag aga gat gat cct aaa aat cca ctg acc att tac aac att acc gca			864
Lys Arg Asp Asp Pro Lys Asn Pro Leu Thr Ile Tyr Asn Ile Thr Ala			
	275	280	285
aca ttg gac ggc aac cgc ttt acc ggc agt gcc aaa gtt agc acc gag			912
Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Ser Thr Glu			
	290	295	300
gtg aag acg caa cac gct gat aaa gaa tat ttg ttt ttc cat acc gat			960
Val Lys Thr Gln His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr Asp			
305	310	315	320
gcc gat cag cgg ctt gag ggc ggt ttt ttc ggc gat aac gga gaa gag			1008
Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Asn Gly Glu Glu			
	325	330	335
ctt gcc ggg cgg ttt atc agt aac gac aac agc gta ttc ggc gtg ttc			1056
Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe			
	340	345	350
gca ggc aaa caa aaa aca gag aca gca aac gca tca gat aca aat cct			1104
Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn Pro			
	355	360	365
gcc ctg ccg tct gga aaa cac acc aaa atc ttg gat tct cta aaa att			1152

Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile	
370 375 380	
tcc gtt gac gag gcg act gat gac cat gcc cgt aag ttt gcc att tcc	1200
Ser Val Asp Glu Ala Thr Asp Asp His Ala Arg Lys Phe Ala Ile Ser	
385 390 395 400	
act atg ccc gat ttt ggt cat ccc gac aaa ctt ctt gtc gaa ggg cgt	1248
Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly Arg	
405 410 415	
gaa att cct ttg gtt agc caa gag aaa acc atc gag ctt gcc gac ggc	1296
Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly	
420 425 430	
agg'aaa atg acc atc cgt gct tgt tgc gat ttt ctg acc tat gtg aaa	1344
Arg Lys Met Thr Ile Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys	
435 440 445	
ctc gga cgg ata aaa acc gac cgc ccc gcc gtc aaa ccg aag gcg cag	1392
Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Val Lys Pro Lys Ala Gln	
450 455 460	
gat gaa gag gat tcg gac att gat aat ggc gaa gaa agc gaa gac gaa	1440
Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu	
465 470 475 480	
att tcc gaa gat gat aac ggc gaa gat gaa gtc acc gaa gaa gag gaa	1488
Ile Ser Glu Asp Asp Asn Gly Glu Asp Glu Val Thr Glu Glu Glu Glu	
485 490 495	
gct gaa gaa acc gaa gaa gaa act gat gaa gac gaa gag gaa gaa ccc	1536
Ala Glu Glu Thr Glu Glu Glu Thr Asp Glu Asp Glu Glu Glu Glu Pro	
500 505 510	
gaa gaa act gaa gaa act gaa gaa act gaa gaa act gaa gaa act gaa	1584
Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu	
515 520 525	
gaa act gaa gaa aaa tcg ccg aca gaa gaa ggc aac ggc ggt tca ggc	1632
Glu Thr Glu Glu Lys Ser Pro Thr Glu Glu Gly Asn Gly Gly Ser Gly	
530 535 540	

agc atc ctg ccc act ccg gaa gcc tct aaa ggc agg gac atc gac ctt 1680  
 Ser Ile Leu Pro Thr Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu  
 545 550 555 560

ttc ctg aaa ggt atc cgc acg gcg gaa gcc gac att ccg caa att gga 1728  
Phe Leu Lys Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Ile Gly  
565 570 575

aaa gca cgc tat acc ggc act tgg gaa gcg cgt atc ggc gtg ccg gat 1776  
Lys Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Val Pro Asp  
580 585 590

aag aaa ggc gaa cag cta gat ggc act acg tcc att caa aag gat agc 1824  
Lys Lys Gly Glu Gln Leu Asp Gly Thr Thr Ser Ile Gln Lys Asp Ser  
595 600 605

tat gcg aat caa gcg gca aaa gca gaa ttt gac gtt gat ttt ggt gcg 1872  
Tyr Ala Asn Gln Ala Ala Lys Ala Glu Phe Asp Val Asp Phe Gly Ala  
610 615 620

aag tcg ctt tca ggt aag ttg aca gaa aaa aat gat aca cac ccc gct 1920  
Lys Ser Leu Ser Gly Lys Leu Thr Glu Lys Asn Asp Thr His Pro Ala  
625 630 635 640

ttt tat att gaa aaa ggt gtg att gat ggc aac ggt ttc cac gct ttg 1968  
Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala Leu  
645 650 655

gcg cgt act cgt gaa aat ggt gtt gat ttg tct ggg caa ggt tcg act 2016  
Ala Arg Thr Arg Glu Asn Gly Val Asp Leu Ser Gly Gln Gly Ser Thr  
660 665 670

aat ccc caa agt ttt aaa gcc agt aat ctt ctc gta gaa gga gga ttt 2064  
Asn Pro Gln Ser Phe Lys Ala Ser Asn Leu Leu Val Glu Gly Gly Phe  
675 680 685

tat ggt ccg cag gcg gca gag ttg ggt ggt aat att atc gac agt gac 2112  
Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser Asp  
690 695 700

cgg aaa atc ggc gtg gta ttc ggt gcg aag aaa gat atg cag gag gtg 2160  
Arg Lys Ile Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val  
705 710 715 720

gaa aaa tga  
Glu Lys

2169

<210> 4  
<211> 722  
<212> PRT  
<213> Neisseria meningitidis strain M981

<400> 4  
Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu  
1 5 10 15  
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser  
20 25 30  
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr  
35 40 45  
Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Gln Pro  
50 55 60  
Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His  
65 70 75 80  
Arg Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys  
85 90 95  
Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Glu  
100 105 110  
Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asn Pro Glu  
115 120 125  
Ala Ser Ile Thr Thr Ser Glu Asn Glu Asn Lys Lys Tyr Asn Tyr Arg  
130 135 140  
Phe Val Ser Ala Gly Tyr Val Phe Thr Lys Asn Gly Lys Asp Glu Ile  
145 150 155 160  
Glu Lys Thr Ser Asp Glu Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp  
165 170 175  
Gly Phe Val Tyr Tyr Leu Gly Glu His Pro Ser Gln Ser Leu Pro Ser  
180 185 190  
Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala  
195 200 205  
Ile Arg His Arg Arg Gly Lys Gly Val Ser Ser Val Asp Leu Gly Tyr  
210 215 220  
Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Ala Ser Tyr Glu Ala Arg  
225 230 235 240  
Asp Ala Asp Gly Arg Glu Lys His Pro Ala Glu Tyr Thr Val Asn Phe

	245		250		255
Asp Lys Lys Asn Leu Glu Gly Lys Leu Ile Lys Asn Gln Tyr Val Gln					
	260		265		270
Lys Arg Asp Asp Pro Lys Asn Pro Leu Thr Ile Tyr Asn Ile Thr Ala					
	275		280		285
Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Ser Thr Glu					
	290		295		300
Val Lys Thr Gln His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr Asp					
305		310		315	320
Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Asn Gly Glu Glu					
	325		330		335
Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe					
	340		345		350
Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn Pro					
	355		360		365
Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile					
	370		375		380
Ser Val Asp Glu Ala Thr Asp Asp His Ala Arg Lys Phe Ala Ile Ser					
385		390		395	400
Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly Arg					
	405		410		415
Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly					
	420		425		430
Arg Lys Met Thr Ile Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys					
	435		440		445
Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Val Lys Pro Lys Ala Gln					
	450		455		460
Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu					
465		470		475	480
Ile Ser Glu Asp Asp Asn Gly Glu Asp Glu Val Thr Glu Glu Glu Glu					
	485		490		495
Ala Glu Glu Thr Glu Glu Glu Thr Asp Glu Asp Glu Glu Glu Glu Pro					
	500		505		510
Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Thr Glu					
	515		520		525
Glu Thr Glu Glu Lys Ser Pro Thr Glu Glu Gly Asn Gly Gly Ser Gly					
	530		535		540
Ser Ile Leu Pro Thr Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu					
545		550		555	560
Phe Leu Lys Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Ile Gly					
	565		570		575
Lys Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Val Pro Asp					
	580		585		590

Lys	Lys	Gly	Glu	Gln	Leu	Asp	Gly	Thr	Thr	Ser	Ile	Gln	Lys	Asp	Ser
		595					600					605			
Tyr	Ala	Asn	Gln	Ala	Ala	Lys	Ala	Glu	Phe	Asp	Val	Asp	Phe	Gly	Ala
		610				615					620				
Lys	Ser	Leu	Ser	Gly	Lys	Leu	Thr	Glu	Lys	Asn	Asp	Thr	His	Pro	Ala
		625			630					635				640	
Phe	Tyr	Ile	Glu	Lys	Gly	Val	Ile	Asp	Gly	Asn	Gly	Phe	His	Ala	Leu
				645					650					655	
Ala	Arg	Thr	Arg	Glu	Asn	Gly	Val	Asp	Leu	Ser	Gly	Gln	Gly	Ser	Thr
			660					665				670			
Asn	Pro	Gln	Ser	Phe	Lys	Ala	Ser	Asn	Leu	Leu	Val	Glu	Gly	Gly	Phe
		675				680					685				
Tyr	Gly	Pro	Gln	Ala	Ala	Glu	Leu	Gly	Gly	Asn	Ile	Ile	Asp	Ser	Asp
		690				695				700					
Arg	Lys	Ile	Gly	Val	Val	Phe	Gly	Ala	Lys	Lys	Asp	Met	Gln	Glu	Val
				710						715				720	
Glu	Lys														

<210> 5  
 <211> 2226  
 <212> DNA  
 <213> Neisseria meningitidis strain H44/76

<220> .  
 <221> CDS  
 <222> (1)...(2223)

<400> 5

atg	tgt	aaa	ccg	aat	tat	ggc	ggc	att	gtc	ttg	ttg	ccc	tta	ctt	ttg	48
Met	Cys	Lys	Pro	Asn	Tyr	Gly	Gly	Ile	Val	Leu	Leu	Pro	Leu	Leu	Leu	
1				5				10				15				
gca	tct	tgt	att	ggc	ggc	aat	ttc	ggc	gtg	cag	cct	gtt	gtc	gaa	tca	96
Ala	Ser	Cys	Ile	Gly	Gly	Asn	Phe	Gly	Val	Gln	Pro	Val	Val	Glu	Ser	
			20					25				30				
acg	ccg	acc	gcg	tac	ccc	gtc	act	ttc	aag	tct	aag	gac	gtt	ccc	act	144
Thr	Pro	Thr	Ala	Tyr	Pro	Val	Thr	Phe	Lys	Ser	Lys	Asp	Val	Pro	Thr	
		35					40					45				
ccg	ccc	cct	gcc	aaa	cct	tct	ata	gaa	acc	acg	ccg	gtg	ccg	tca	acc	192

Pro	Pro	Pro	Ala	Lys	Pro	Ser	Ile	Glu	Thr	Thr	Pro	Val	Pro	Ser	Thr		
50						55					60						
ggg	cct	gcc	gtc	ggt	gcg	gca	atg	cgg	ctg	ttg	agg	cgg	att	ttc	gca	240	
Gly	Pro	Ala	Val	Gly	Ala	Ala	Met	Arg	Leu	Leu	Arg	Arg	Ile	Phe	Ala		
65					70					75				80			
act	tct	gat	aag	gtt	ggc	aat	gat	ttt	cca	aat	agc	aaa	caa	gca	gaa	288	
Thr	Ser	Asp	Lys	Val	Gly	Asn	Asp	Phe	Pro	Asn	Ser	Lys	Gln	Ala	Glu		
			85					90					95				
gaa	aag	ctg	tcg	ttt	aaa	gaa	ggt	gat	gtt	ctg	ttt	tta	tac	ggt	tca	336	
Glu	Lys	Leu	Ser	Phe	Lys	Glu	Gly	Asp	Val	Leu	Phe	Leu	Tyr	Gly	Ser		
			100					105					110				
aaa	aaa	gat	aaa	ctt	cag	tgg	ctt	aag	gat	aaa	att	cat	caa	cgc	aat	384	
Lys	Lys	Asp	Lys	Leu	Gln	Trp	Leu	Lys	Asp	Lys	Ile	His	Gln	Arg	Asn		
		115					120					125					
cct	aat	gta	gaa	att	agg	aca	tca	gaa	aat	gaa	aat	aaa	aaa	tat	ggt	432	
Pro	Asn	Val	Glu	Ile	Arg	Thr	Ser	Glu	Asn	Glu	Asn	Lys	Lys	Tyr	Gly		
	130						135					140					
tat	gaa	ttt	gtg	gat	gcc	ggt	tat	gta	tat	act	aaa	aac	gga	aca	gat	480	
Tyr	Glu	Phe	Val	Asp	Ala	Gly	Tyr	Val	Tyr	Thr	Lys	Asn	Gly	Thr	Asp		
145					150					155				160			
gaa	att	gag	tgg	act	tca	aat	cgc	aag	cag	ttt	tct	aat	cgt	ttt	ggc	528	
Glu	Ile	Glu	Trp	Thr	Ser	Asn	Arg	Lys	Gln	Phe	Ser	Asn	Arg	Phe	Gly		
			165						170				175				
tac	gac	ggt	ttt	gta	tat	tat	tcc	gga	gaa	cat	cct	tcc	caa	tct	tta	576	
Tyr	Asp	Gly	Phe	Val	Tyr	Tyr	Ser	Gly	Glu	His	Pro	Ser	Gln	Ser	Leu		
			180					185					190				
ccg	agc	gcg	gga	acg	gtg	caa	tat	tcc	ggt	aac	tgg	caa	tat	atg	acc	624	
Pro	Ser	Ala	Gly	Thr	Val	Gln	Tyr	Ser	Gly	Asn	Trp	Gln	Tyr	Met	Thr		
		195					200					205					
gat	gcc	ata	cgt	cat	cga	aca	gga	aaa	gca	gga	gat	cct	agc	gaa	gat	672	
Asp	Ala	Ile	Arg	His	Arg	Thr	Gly	Lys	Ala	Gly	Asp	Pro	Ser	Glu	Asp		
	210					215					220						



ttg	ggt	tat	ctc	ggt	tat	tac	ggt	caa	aat	gtc	gga	gca	act	tct	tat	720
Leu	Gly	Tyr	Leu	Val	Tyr	Tyr	Gly	Gln	Asn	Val	Gly	Ala	Thr	Ser	Tyr	
225					230					235					240	
gct	gcg	act	gcc	gac	gac	cgg	gag	gga	aaa	cat	cct	gcc	gaa	tat	acg	768
Ala	Ala	Thr	Ala	Asp	Asp	Arg	Glu	Gly	Lys	His	Pro	Ala	Glu	Tyr	Thr	
				245					250					255		
gtt	gat	ttc	gat	aag	aaa	act	ttg	acg	ggt	caa	tta	att	aaa	aat	cag	816
Val	Asp	Phe	Asp	Lys	Lys	Thr	Leu	Thr	Gly	Gln	Leu	Ile	Lys	Asn	Gln	
				260				265					270			
tat	gtg	caa	aag	aaa	acc	gat	gaa	aag	aaa	cca	ctg	acc	att	tac	gac	864
Tyr	Val	Gln	Lys	Lys	Thr	Asp	Glu	Lys	Lys	Pro	Leu	Thr	Ile	Tyr	Asp	
		275					280					285				
att	acc	gca	aca	ttg	gac	ggc	aac	cgc	ttt	acc	ggc	agt	gcc	aaa	gtt	912
Ile	Thr	Ala	Thr	Leu	Asp	Gly	Asn	Arg	Phe	Thr	Gly	Ser	Ala	Lys	Val	
	290					295					300					
aac	acc	gag	ttg	aag	acg	agc	cac	gct	gat	aaa	gag	cat	ttg	ttt	ttc	960
Asn	Thr	Glu	Leu	Lys	Thr	Ser	His	Ala	Asp	Lys	Glu	His	Leu	Phe	Phe	
305					310					315					320	
cat	acc	gat	gcc	gat	cag	cgg	ctt	gag	ggc	ggt	ttt	ttc	ggc	gat	aag	1008
His	Thr	Asp	Ala	Asp	Gln	Arg	Leu	Glu	Gly	Gly	Phe	Phe	Gly	Asp	Lys	
				325					330					335		
ggg	gaa	gag	ctt	gcc	gga	cgg	ttt	atc	agc	aac	gac	aac	agc	gta	ttc	1056
Gly	Glu	Glu	Leu	Ala	Gly	Arg	Phe	Ile	Ser	Asn	Asp	Asn	Ser	Val	Phe	
			340					345					350			
ggc	gta	ttc	gca	ggc	aaa	aaa	aca	aac	gca	tca	aac	gca	gca	gat	aca	1104
Gly	Val	Phe	Ala	Gly	Lys	Lys	Thr	Asn	Ala	Ser	Asn	Ala	Ala	Asp	Thr	
		355					360					365				
aat	cct	gct	atg	ccg	tct	gaa	aaa	cac	acc	aaa	atc	ttg	gat	tct	ctg	1152
Asn	Pro	Ala	Met	Pro	Ser	Glu	Lys	His	Thr	Lys	Ile	Leu	Asp	Ser	Leu	
	370					375					380					
aaa	att	tcc	gtt	gac	gag	gcg	acg	gat	aaa	aat	gcc	cgc	ccg	ttt	gcc	1200
Lys	Ile	Ser	Val	Asp	Glu	Ala	Thr	Asp	Lys	Asn	Ala	Arg	Pro	Phe	Ala	
385					390					395					400	

att tcc cct ctg ccc gat ttt ggc cat ccc gac aaa ctc ctt gtc gaa	1248
Ile Ser Pro Leu Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu	
405 410 415	
ggg cgt gaa att cct ttg gtt agc caa gag aaa acc atc gag ctt gcc	1296
Gly Arg Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala	
420 425 430	
gac ggc agg aaa atg acc gtc cgt gct tgt tgc gat ttt ctg acc tat	1344
Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr	
435 440 445	
gtg aaa ctc gga cgg ata aaa act gac cgc cca gca agt aaa cca aag	1392
Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys Pro Lys	
450 455 460	
gcg gaa gat aaa ggg aag gat gaa gag gat aca ggc gtt ggt aac gac	1440
Ala Glu Asp Lys Gly Lys Asp Glu Glu Asp Thr Gly Val Gly Asn Asp	
465 470 475 480	
gaa gaa ggc acg gaa gat gaa gcc gca gaa ggc agc gaa gga ggc gaa	1488
Glu Glu Gly Thr Glu Asp Glu Ala Ala Glu Gly Ser Glu Gly Gly Glu	
485 490 495	
gac gaa atc ggc gat gaa gga gga ggt gcg gaa gac gaa gcc gca gaa	1536
Asp Glu Ile Gly Asp Glu Gly Gly Gly Ala Glu Asp Glu Ala Ala Glu	
500 505 510	
aac gaa ggc ggc gaa gaa gac gaa gct gaa gaa cct gaa gaa ccc gaa	1584
Asn Glu Gly Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Pro Glu	
515 520 525	
gaa gaa tcg ccg gca gaa ggc ggc ggt ggt ggt tca gac ggc atc ctg	1632
Glu Glu Ser Pro Ala Glu Gly Gly Gly Gly Gly Ser Asp Gly Ile Leu	
530 535 540	
ccc gct ccg gaa gct cct aaa ggc agg gat atc gac ctt ttc ctg aaa	1680
Pro Ala Pro Glu Ala Pro Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys	
545 550 555 560	
ggt atc cgc acg gcg gaa gcc gac att ccg caa act gga aaa gca cgc	1728
Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Thr Gly Lys Ala Arg	

565	570	575	
tat acc ggc act tgg gaa gcg cgt atc agc aaa ccc att caa tgg gac			1776
Tyr Thr Gly Thr Trp Glu Ala Arg Ile Ser Lys Pro Ile Gln Trp Asp			
580	585	590	
aat cat gcg gat aaa aaa gcg gca aaa gca gaa ttt gac gtt gat ttc			1824
Asn His Ala Asp Lys Lys Ala Ala Lys Ala Glu Phe Asp Val Asp Phe			
595	600	605	
ggc gag aaa tcg att tcc gga acg ctg acg gag aaa aac ggt gta caa			1872
Gly Glu Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys Asn Gly Val Gln			
610	615	620	
cct gct ttc cat att gaa aac ggc gtg att gag ggc aat ggt ttc cac			1920
Pro Ala Phe His Ile Glu Asn Gly Val Ile Glu Gly Asn Gly Phe His			
625	630	635	640
gcg aca gcg cgc act cgg gat aac ggc atc aat ctt tcg gga aat gat			1968
Ala Thr Ala Arg Thr Arg Asp Asn Gly Ile Asn Leu Ser Gly Asn Asp			
645	650	655	
tcg act aat cct cca agt ttc aaa gcc aat aat ctt ctt gta aca ggc			2016
Ser Thr Asn Pro Pro Ser Phe Lys Ala Asn Asn Leu Leu Val Thr Gly			
660	665	670	
ggc ttt tac ggc ccg cag gcg gag gaa ttg ggc ggt act att ttc aat			2064
Gly Phe Tyr Gly Pro Gln Ala Glu Glu Leu Gly Gly Thr Ile Phe Asn			
675	680	685	
aat gat ggg aaa tct ctt ggt ata act gaa gat act gaa aat gaa gct			2112
Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Asp Thr Glu Asn Glu Ala			
690	695	700	
gaa gct gaa gtt gaa aat gaa gct ggt gtt ggc gaa cag tta aaa cct			2160
Glu Ala Glu Val Glu Asn Glu Ala Gly Val Gly Glu Gln Leu Lys Pro			
705	710	715	720
gaa gct aaa ccc caa ttc ggc gtg gta ttc ggt gcg aag aaa gat aat			2208
Glu Ala Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn			
725	730	735	
aaa gag gtg gaa aaa tga			2226

Lys Glu Val Glu Lys  
740

<210> 6

<211> 741

<212> PRT

<213> Neisseria meningitidis strain H44/76

<400> 6

Met	Cys	Lys	Pro	Asn	Tyr	Gly	Gly	Ile	Val	Leu	Leu	Pro	Leu	Leu	Leu
1				5					10					15	
Ala	Ser	Cys	Ile	Gly	Gly	Asn	Phe	Gly	Val	Gln	Pro	Val	Val	Glu	Ser
			20					25					30		
Thr	Pro	Thr	Ala	Tyr	Pro	Val	Thr	Phe	Lys	Ser	Lys	Asp	Val	Pro	Thr
			35				40					45			
Pro	Pro	Pro	Ala	Lys	Pro	Ser	Ile	Glu	Thr	Thr	Pro	Val	Pro	Ser	Thr
			50				55					60			
Gly	Pro	Ala	Val	Gly	Ala	Ala	Met	Arg	Leu	Leu	Arg	Arg	Ile	Phe	Ala
65					70					75					80
Thr	Ser	Asp	Lys	Val	Gly	Asn	Asp	Phe	Pro	Asn	Ser	Lys	Gln	Ala	Glu
				85					90					95	
Glu	Lys	Leu	Ser	Phe	Lys	Glu	Gly	Asp	Val	Leu	Phe	Leu	Tyr	Gly	Ser
			100					105						110	
Lys	Lys	Asp	Lys	Leu	Gln	Trp	Leu	Lys	Asp	Lys	Ile	His	Gln	Arg	Asn
			115				120						125		
Pro	Asn	Val	Glu	Ile	Arg	Thr	Ser	Glu	Asn	Glu	Asn	Lys	Lys	Tyr	Gly
			130				135						140		
Tyr	Glu	Phe	Val	Asp	Ala	Gly	Tyr	Val	Tyr	Thr	Lys	Asn	Gly	Thr	Asp
145					150					155					160
Glu	Ile	Glu	Trp	Thr	Ser	Asn	Arg	Lys	Gln	Phe	Ser	Asn	Arg	Phe	Gly
				165					170					175	
Tyr	Asp	Gly	Phe	Val	Tyr	Tyr	Ser	Gly	Glu	His	Pro	Ser	Gln	Ser	Leu
			180					185						190	
Pro	Ser	Ala	Gly	Thr	Val	Gln	Tyr	Ser	Gly	Asn	Trp	Gln	Tyr	Met	Thr
			195					200						205	
Asp	Ala	Ile	Arg	His	Arg	Thr	Gly	Lys	Ala	Gly	Asp	Pro	Ser	Glu	Asp
			210				215				220				
Leu	Gly	Tyr	Leu	Val	Tyr	Tyr	Gly	Gln	Asn	Val	Gly	Ala	Thr	Ser	Tyr
225					230					235					240
Ala	Ala	Thr	Ala	Asp	Asp	Arg	Glu	Gly	Lys	His	Pro	Ala	Glu	Tyr	Thr
				245					250					255	
Val	Asp	Phe	Asp	Lys	Lys	Thr	Leu	Thr	Gly	Gln	Leu	Ile	Lys	Asn	Gln

			260					265					270			
Tyr	Val	Gln	Lys	Lys	Thr	Asp	Glu	Lys	Lys	Pro	Leu	Thr	Ile	Tyr	Asp	
		275					280					285				
Ile	Thr	Ala	Thr	Leu	Asp	Gly	Asn	Arg	Phe	Thr	Gly	Ser	Ala	Lys	Val	
		290				295					300					
Asn	Thr	Glu	Leu	Lys	Thr	Ser	His	Ala	Asp	Lys	Glu	His	Leu	Phe	Phe	
305					310					315					320	
His	Thr	Asp	Ala	Asp	Gln	Arg	Leu	Glu	Gly	Gly	Phe	Phe	Gly	Asp	Lys	
				325					330					335		
Gly	Glu	Glu	Leu	Ala	Gly	Arg	Phe	Ile	Ser	Asn	Asp	Asn	Ser	Val	Phe	
			340				345						350			
Gly	Val	Phe	Ala	Gly	Lys	Lys	Thr	Asn	Ala	Ser	Asn	Ala	Ala	Asp	Thr	
		355				360					365					
Asn	Pro	Ala	Met	Pro	Ser	Glu	Lys	His	Thr	Lys	Ile	Leu	Asp	Ser	Leu	
		370				375					380					
Lys	Ile	Ser	Val	Asp	Glu	Ala	Thr	Asp	Lys	Asn	Ala	Arg	Pro	Phe	Ala	
385				390						395					400	
Ile	Ser	Pro	Leu	Pro	Asp	Phe	Gly	His	Pro	Asp	Lys	Leu	Leu	Val	Glu	
			405					410						415		
Gly	Arg	Glu	Ile	Pro	Leu	Val	Ser	Gln	Glu	Lys	Thr	Ile	Glu	Leu	Ala	
			420				425						430			
Asp	Gly	Arg	Lys	Met	Thr	Val	Arg	Ala	Cys	Cys	Asp	Phe	Leu	Thr	Tyr	
		435				440						445				
Val	Lys	Leu	Gly	Arg	Ile	Lys	Thr	Asp	Arg	Pro	Ala	Ser	Lys	Pro	Lys	
		450				455					460					
Ala	Glu	Asp	Lys	Gly	Lys	Asp	Glu	Glu	Asp	Thr	Gly	Val	Gly	Asn	Asp	
465					470					475					480	
Glu	Glu	Gly	Thr	Glu	Asp	Glu	Ala	Ala	Glu	Gly	Ser	Glu	Gly	Gly	Glu	
			485						490					495		
Asp	Glu	Ile	Gly	Asp	Glu	Gly	Gly	Gly	Ala	Glu	Asp	Glu	Ala	Ala	Glu	
			500				505						510			
Asn	Glu	Gly	Gly	Glu	Glu	Asp	Glu	Ala	Glu	Glu	Pro	Glu	Glu	Pro	Glu	
		515				520						525				
Glu	Glu	Ser	Pro	Ala	Glu	Gly	Gly	Gly	Gly	Gly	Ser	Asp	Gly	Ile	Leu	
		530				535					540					
Pro	Ala	Pro	Glu	Ala	Pro	Lys	Gly	Arg	Asp	Ile	Asp	Leu	Phe	Leu	Lys	
545					550					555					560	
Gly	Ile	Arg	Thr	Ala	Glu	Ala	Asp	Ile	Pro	Gln	Thr	Gly	Lys	Ala	Arg	
			565						570					575		
Tyr	Thr	Gly	Thr	Trp	Glu	Ala	Arg	Ile	Ser	Lys	Pro	Ile	Gln	Trp	Asp	
			580					585					590			
Asn	His	Ala	Asp	Lys	Lys	Ala	Ala	Lys	Ala	Glu	Phe	Asp	Val	Asp	Phe	
		595					600									

Gly Glu Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys Asn Gly Val Gln  
 610 615 620  
 Pro Ala Phe His Ile Glu Asn Gly Val Ile Glu Gly Asn Gly Phe His  
 625 630 635 640  
 Ala Thr Ala Arg Thr Arg Asp Asn Gly Ile Asn Leu Ser Gly Asn Asp  
 645 650 655  
 Ser Thr Asn Pro Pro Ser Phe Lys Ala Asn Asn Leu Leu Val Thr Gly  
 660 665 670  
 Gly Phe Tyr Gly Pro Gln Ala Glu Glu Leu Gly Gly Thr Ile Phe Asn  
 675 680 685  
 Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Asp Thr Glu Asn Glu Ala  
 690 695 700  
 Glu Ala Glu Val Glu Asn Glu Ala Gly Val Gly Glu Gln Leu Lys Pro  
 705 710 715 720  
 Glu Ala Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn  
 725 730 735  
 Lys Glu Val Glu Lys  
 740

<210> 7

<211> 2262

<212> DNA

<213> Neisseria meningitidis strain M990

<220>

<221> CDS

<222> (1)...(2259)

<400> 7

atg tgt aaa ccg aat tat ggc ggc att gtc ttg ttg ccc tta ctt tta	48
Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu	
1 5 10 15	
gca tct tgt atc ggc ggc aat ttc ggc gta cag cct gtt gtc gaa tca	96
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser	
20 25 30	
acg ccg acc gcg cca act ctg tca gat tcc aaa tct tcc aat cct gcg	144
Thr Pro Thr Ala Pro Thr Leu Ser Asp Ser Lys Ser Ser Asn Pro Ala	
35 40 45	
gat aag cct gct cca gct cct gcc gag cct tcg gta gaa atc acg ccg	192

Asp	Lys	Pro	Ala	Pro	Ala	Pro	Ala	Glu	Pro	Ser	Val	Glu	Ile	Thr	Pro		
50						55					60						
gtc	aag	cgg	ccc	gcc	gtc	ggg	gcg	gca	atg	cgg	ctg	cca	agg	cgg	aat	240	
Val	Lys	Arg	Pro	Ala	Val	Gly	Ala	Ala	Met	Arg	Leu	Pro	Arg	Arg	Asn		
65					70					75					80		
atc	gca	act	ttt	gat	aaa	aat	ggg	aat	gaa	att	ccc	aat	agt	aag	cag	288	
Ile	Ala	Thr	Phe	Asp	Lys	Asn	Gly	Asn	Glu	Ile	Pro	Asn	Ser	Lys	Gln		
				85					90					95			
gca	gag	gag	tat	ctg	ccg	ctc	aaa	gag	aag	gat	atc	ctg	ttt	tta	gac	336	
Ala	Glu	Glu	Tyr	Leu	Pro	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Phe	Leu	Asp		
			100					105					110				
ggg	acg	ccg	aaa	gaa	cag	gct	gac	aaa	ctt	aaa	aag	gaa	atc	aac	gga	384	
Gly	Thr	Pro	Lys	Glu	Gln	Ala	Asp	Lys	Leu	Lys	Lys	Glu	Ile	Asn	Gly		
		115					120					125					
cgg	cat	cct	aat	gca	cca	atc	tac	acg	tcc	gat	tta	aaa	gat	gat	gcg	432	
Arg	His	Pro	Asn	Ala	Pro	Ile	Tyr	Thr	Ser	Asp	Leu	Lys	Asp	Asp	Ala		
	130					135				140							
tat	caa	tat	aaa	tat	gtc	cgg	gcc	gga	tat	gtt	tat	act	aga	tat	gga	480	
Tyr	Gln	Tyr	Lys	Tyr	Val	Arg	Ala	Gly	Tyr	Val	Tyr	Thr	Arg	Tyr	Gly		
145					150					155					160		
aca	gat	gaa	atc	gaa	cag	aac	tca	ggc	ggg	aag	cgg	gtt	acc	cac	cgc	528	
Thr	Asp	Glu	Ile	Glu	Gln	Asn	Ser	Gly	Gly	Lys	Arg	Val	Thr	His	Arg		
				165					170					175			
tta	ggg	tat	gac	ggg	ttt	gta	tat	tat	tcc	gga	gaa	cgt	cct	tcc	caa	576	
Leu	Gly	Tyr	Asp	Gly	Phe	Val	Tyr	Tyr	Ser	Gly	Glu	Arg	Pro	Ser	Gln		
			180					185					190				
tct	tta	ccg	agt	gcg	gga	acg	gtg	gaa	tat	tct	ggg	aac	tgg	caa	tat	624	
Ser	Leu	Pro	Ser	Ala	Gly	Thr	Val	Glu	Tyr	Ser	Gly	Asn	Trp	Gln	Tyr		
		195					200					205					
atg	acc	gat	gcc	aaa	cgt	cat	cga	gca	ggg	cag	gcg	gtt	ggc	att	gac	672	
Met	Thr	Asp	Ala	Lys	Arg	His	Arg	Ala	Gly	Gln	Ala	Val	Gly	Ile	Asp		
	210					215					220						

aat	ttg	ggt	tat	atc	aca	ttt	tat	ggt	aac	gat	ggt	ggt	gca	act	tct	720
Asn	Leu	Gly	Tyr	Ile	Thr	Phe	Tyr	Gly	Asn	Asp	Val	Gly	Ala	Thr	Ser	
225					230					235					240	
tat	gcg	gct	aag	gat	gtc	gac	gaa	agg	gaa	aag	cat	cct	gcc	aaa	tat	768
Tyr	Ala	Ala	Lys	Asp	Val	Asp	Glu	Arg	Glu	Lys	His	Pro	Ala	Lys	Tyr	
				245					250					255		
acg	gtt	gat	ttt	gat	aac	aaa	acc	atg	aat	ggc	aag	ctg	att	aaa	aat	816
Thr	Val	Asp	Phe	Asp	Asn	Lys	Thr	Met	Asn	Gly	Lys	Leu	Ile	Lys	Asn	
			260					265					270			
cag	tat	gtg	cga	aat	aaa	aaa	gat	gaa	ccc	aaa	aaa	ccg	ctg	acc	att	864
Gln	Tyr	Val	Arg	Asn	Lys	Lys	Asp	Glu	Pro	Lys	Lys	Pro	Leu	Thr	Ile	
		275					280					285				
tac	gac	att	act	gca	aaa	ttg	gac	ggc	aac	cgc	ttt	acc	ggc	agt	gcc	912
Tyr	Asp	Ile	Thr	Ala	Lys	Leu	Asp	Gly	Asn	Arg	Phe	Thr	Gly	Ser	Ala	
	290					295				300						
aag	gtc	aat	cct	gat	tta	gcg	aaa	aac	ctt	gcc	ggt	aat	gag	cgt	ttg	960
Lys	Val	Asn	Pro	Asp	Leu	Ala	Lys	Asn	Leu	Ala	Gly	Asn	Glu	Arg	Leu	
305					310					315					320	
ttt	ttc	cat	gcc	gat	gcc	gat	cag	cgg	ctt	gag	ggc	ggt	ttt	ttc	ggc	1008
Phe	Phe	His	Ala	Asp	Ala	Asp	Gln	Arg	Leu	Glu	Gly	Gly	Phe	Phe	Gly	
			325					330					335			
gat	aac	gga	gaa	gag	ctt	gcc	gga	cgg	ttt	atc	agc	aac	gac	aac	agc	1056
Asp	Asn	Gly	Glu	Glu	Leu	Ala	Gly	Arg	Phe	Ile	Ser	Asn	Asp	Asn	Ser	
			340					345					350			
gta	ttc	ggc	gta	ttc	gca	ggc	aaa	aaa	aca	gag	aca	gca	aac	gca	gca	1104
Val	Phe	Gly	Val	Phe	Ala	Gly	Lys	Lys	Thr	Glu	Thr	Ala	Asn	Ala	Ala	
		355					360					365				
gat	aca	aaa	cct	gcc	ctg	ccg	tct	gga	aaa	cac	acc	aaa	atc	ttg	gat	1152
Asp	Thr	Lys	Pro	Ala	Leu	Pro	Ser	Gly	Lys	His	Thr	Lys	Ile	Leu	Asp	
	370					375					380					
tct	cta	aaa	att	tcc	gtt	gac	gag	gcg	act	gat	ggc	cat	gcc	cgt	aag	1200
Ser	Leu	Lys	Ile	Ser	Val	Asp	Glu	Ala	Thr	Asp	Gly	His	Ala	Arg	Lys	
385					390				395						400	



ttt gcc att tcc tct atg ccc gat ttt ggt cat ccc gac aaa ctt ctt	1248
Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu	
405 410 415	
gtc gaa ggg cgt gaa att cct ttg gta aac gaa gaa caa atc atc aag	1296
Val Glu Gly Arg Glu Ile Pro Leu Val Asn Glu Glu Gln Ile Ile Lys	
420 425 430	
ctt gcc gac ggc agg aaa atg acc gtc cgt gct tgt tgc gac ttt ttg	1344
Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu	
435 440 445	
acc tat gtg aaa ctc gga cgg ata aaa acc gat cgc ccg gca agt aaa	1392
Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys	
450 455 460	
cca aag gcg gaa gat aaa ggg gag gat gaa gag ggt gca ggc gtt gat	1440
Pro Lys Ala Glu Asp Lys Gly Glu Asp Glu Glu Gly Ala Gly Val Asp	
465 470 475 480	
aac gac gaa gaa agc gaa gac gaa gcc gta gaa gac gaa ggc ggc gaa	1488
Asn Asp Glu Glu Ser Glu Asp Glu Ala Val Glu Asp Glu Gly Gly Glu	
485 490 495	
gaa gac gaa act tcc gaa gag gat aat ggc gaa gac gaa gaa gca acc	1536
Glu Asp Glu Thr Ser Glu Glu Asp Asn Gly Glu Asp Glu Glu Ala Thr	
500 505 510	
gcc gaa gaa gaa acc gaa gaa gtt gat gaa gcc gaa gag gag gaa gtt	1584
Ala Glu Glu Glu Thr Glu Glu Val Asp Glu Ala Glu Glu Glu Glu Val	
515 520 525	
gaa gaa ccc gaa gaa aaa tcg ccg gca gaa ggc aac ggc ggt tca ggc	1632
Glu Glu Pro Glu Glu Lys Ser Pro Ala Glu Gly Asn Gly Gly Ser Gly	
530 535 540	
agc atc ctg cct gcc cta gaa gcc tct aaa ggc agg gac atc gac ctt	1680
Ser Ile Leu Pro Ala Leu Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu	
545 550 555 560	
ttc ctg aaa ggt atc cgc acg gca gaa acg gat att ccg caa agc gga	1728
Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asp Ile Pro Gln Ser Gly	

565	570	575	
acg gcg cat tat acc ggc act tgg gaa gcg cgt atc ggc aaa ccc att			1776
Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro Ile			
580	585	590	
caa tgg gac aat cag gcg gat gaa aaa gcg gca aaa gca gaa ttt acc			1824
Gln Trp Asp Asn Gln Ala Asp Glu Lys Ala Ala Lys Ala Glu Phe Thr			
595	600	605	
gtt gat ttc gac aag aaa tcg att tcc gga aag ctg acg gag caa aac			1872
Val Asp Phe Asp Lys Lys Ser Ile Ser Gly Lys Leu Thr Glu Gln Asn			
610	615	620	
ggc gta gaa cct gct ttc cat att gaa gac ggc aag att gat ggc aac			1920
Gly Val Glu Pro Ala Phe His Ile Glu Asp Gly Lys Ile Asp Gly Asn			
625	630	635	640
ggt ttc cac gcg aca gcg cgc act cgg gag agc ggc atc aat ctt tcg			1968
Gly Phe His Ala Thr Ala Arg Thr Arg Glu Ser Gly Ile Asn Leu Ser			
645	650	655	
gga aat ggt tcg acc gac ccc aaa aca ttc caa gct agt aat ctt cgt			2016
Gly Asn Gly Ser Thr Asp Pro Lys Thr Phe Gln Ala Ser Asn Leu Arg			
660	665	670	
gta gaa gga gga ttt tac ggc ccg cag gcg gcg gaa ttg ggc ggt act			2064
Val Glu Gly Gly Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Thr			
675	680	685	
att ttc aat aat gat ggg aaa tct ctt agt ata act gaa aat att gaa			2112
Ile Phe Asn Asn Asp Gly Lys Ser Leu Ser Ile Thr Glu Asn Ile Glu			
690	695	700	
aat gaa gct gaa gct gaa gtt gaa gtt gaa gct gaa gct gaa gtt gaa			2160
Asn Glu Ala Glu Ala Glu Val Glu Val Glu Ala Glu Ala Glu Val Glu			
705	710	715	720
gtt gaa gct gat gtt ggc aaa cag tta gaa cct gat gaa gtt aaa cac			2208
Val Glu Ala Asp Val Gly Lys Gln Leu Glu Pro Asp Glu Val Lys His			
725	730	735	
aaa ttc ggc gtg gta ttc ggt gcg aag aaa gat atg cag gag gtg gaa			2256

Lys Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu  
740 745 750

aaa tga  
Lys

2262

<210> 8  
<211> 753  
<212> PRT  
<213> Neisseria meningitidis strain M990

<400> 8  
Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu  
1 5 10 15  
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser  
20 25 30  
Thr Pro Thr Ala Pro Thr Leu Ser Asp Ser Lys Ser Ser Asn Pro Ala  
35 40 45  
Asp Lys Pro Ala Pro Ala Pro Ala Glu Pro Ser Val Glu Ile Thr Pro  
50 55 60  
Val Lys Arg Pro Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn  
65 70 75 80  
Ile Ala Thr Phe Asp Lys Asn Gly Asn Glu Ile Pro Asn Ser Lys Gln  
85 90 95  
Ala Glu Glu Tyr Leu Pro Leu Lys Glu Lys Asp Ile Leu Phe Leu Asp  
100 105 110  
Gly Thr Pro Lys Glu Gln Ala Asp Lys Leu Lys Lys Glu Ile Asn Gly  
115 120 125  
Arg His Pro Asn Ala Pro Ile Tyr Thr Ser Asp Leu Lys Asp Asp Ala  
130 135 140  
Tyr Gln Tyr Lys Tyr Val Arg Ala Gly Tyr Val Tyr Thr Arg Tyr Gly  
145 150 155 160  
Thr Asp Glu Ile Glu Gln Asn Ser Gly Gly Lys Arg Val Thr His Arg  
165 170 175  
Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln  
180 185 190  
Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr  
195 200 205  
Met Thr Asp Ala Lys Arg His Arg Ala Gly Gln Ala Val Gly Ile Asp  
210 215 220  
Asn Leu Gly Tyr Ile Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser

225	230	235	240
Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr			
245	250	255	
Thr Val Asp Phe Asp Asn Lys Thr Met Asn Gly Lys Leu Ile Lys Asn			
260	265	270	
Gln Tyr Val Arg Asn Lys Lys Asp Glu Pro Lys Lys Pro Leu Thr Ile			
275	280	285	
Tyr Asp Ile Thr Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala			
290	295	300	
Lys Val Asn Pro Asp Leu Ala Lys Asn Leu Ala Gly Asn Glu Arg Leu			
305	310	315	320
Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly			
325	330	335	
Asp Asn Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser			
340	345	350	
Val Phe Gly Val Phe Ala Gly Lys Lys Thr Glu Thr Ala Asn Ala Ala			
355	360	365	
Asp Thr Lys Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp			
370	375	380	
Ser Leu Lys Ile Ser Val Asp Glu Ala Thr Asp Gly His Ala Arg Lys			
385	390	395	400
Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu			
405	410	415	
Val Glu Gly Arg Glu Ile Pro Leu Val Asn Glu Glu Gln Ile Ile Lys			
420	425	430	
Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu			
435	440	445	
Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys			
450	455	460	
Pro Lys Ala Glu Asp Lys Gly Glu Asp Glu Glu Gly Ala Gly Val Asp			
465	470	475	480
Asn Asp Glu Glu Ser Glu Asp Glu Ala Val Glu Asp Glu Gly Gly Glu			
485	490	495	
Glu Asp Glu Thr Ser Glu Glu Asp Asn Gly Glu Asp Glu Glu Ala Thr			
500	505	510	
Ala Glu Glu Glu Thr Glu Glu Val Asp Glu Ala Glu Glu Glu Glu Val			
515	520	525	
Glu Glu Pro Glu Glu Lys Ser Pro Ala Glu Gly Asn Gly Gly Ser Gly			
530	535	540	
Ser Ile Leu Pro Ala Leu Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu			
545	550	555	560
Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asp Ile Pro Gln Ser Gly			
565	570	575	

Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro Ile  
 580 585 590  
 Gln Trp Asp Asn Gln Ala Asp Glu Lys Ala Ala Lys Ala Glu Phe Thr  
 595 600 605  
 Val Asp Phe Asp Lys Lys Ser Ile Ser Gly Lys Leu Thr Glu Gln Asn  
 610 615 620  
 Gly Val Glu Pro Ala Phe His Ile Glu Asp Gly Lys Ile Asp Gly Asn  
 625 630 635 640  
 Gly Phe His Ala Thr Ala Arg Thr Arg Glu Ser Gly Ile Asn Leu Ser  
 645 650 655  
 Gly Asn Gly Ser Thr Asp Pro Lys Thr Phe Gln Ala Ser Asn Leu Arg  
 660 665 670  
 Val Glu Gly Gly Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Thr  
 675 680 685  
 Ile Phe Asn Asn Asp Gly Lys Ser Leu Ser Ile Thr Glu Asn Ile Glu  
 690 695 700  
 Asn Glu Ala Glu Ala Glu Val Glu Val Glu Ala Glu Ala Glu Val Glu  
 705 710 715 720  
 Val Glu Ala Asp Val Gly Lys Gln Leu Glu Pro Asp Glu Val Lys His  
 725 730 735  
 Lys Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu  
 740 745 750  
 Lys

<210> 9

<211> 2124

<212> DNA

<213> *Neisseria meningitidis* strain 881607

<220>

<221> CDS

<222> (1)...(2121)

<400> 9

atg tgt aaa ccg aat tat ggc ggc att gtc ttg ttg ccc tta ctt ttg 48  
 Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu  
 1 5 10 15

gca tct tgc atc ggc ggc aat ttc ggc gtg cag cct gtt gtc gaa tca 96  
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser  
 20 25 30

acg ccg acc gcg tac ccc gtc act ttc aag tct aag gac gtt ccc act	144
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr	
35 40 45	
tcg cct cct gcc ggg tct tcg gta gaa acc acg ccg gtc aac cga ccc	192
Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Arg Pro	
50 55 60	
gcc gtt ggt gcg gca atg cgg ctg ttg aga cgg aat att gca act tct	240
Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Ile Ala Thr Ser	
65 70 75 80	
gat aag gat ggc aat gat ttt cca aat agc aaa caa gca gaa gaa aag	288
Asp Lys Asp Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu Glu Lys	
85 90 95	
ctg tcg ttt aaa gag gaa gat atc ctg ttt tta tac ggt tcc aaa aaa	336
Leu Ser Phe Lys Glu Glu Asp Ile Leu Phe Leu Tyr Gly Ser Lys Lys	
100 105 110	
gat caa cgt cag cag ctt aaa gat aaa att cgt caa cca aat cct acg	384
Asp Gln Arg Gln Gln Leu Lys Asp Lys Ile Arg Gln Pro Asn Pro Thr	
115 120 125	
gca agc att acc aca tcg gaa aag aaa aat aaa aaa tat gat tat aaa	432
Ala Ser Ile Thr Thr Ser Glu Lys Lys Asn Lys Lys Tyr Asp Tyr Lys	
130 135 140	
ttt gta gat gca ggt tat gta tat act aaa gac gga aaa gat gaa att	480
Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asp Gly Lys Asp Glu Ile	
145 150 155 160	
gag tgg act tca aat tac aag cag tct acc aac cgg ttt ggt tat gac	528
Glu Trp Thr Ser Asn Tyr Lys Gln Ser Thr Asn Arg Phe Gly Tyr Asp	
165 170 175	
ggt ttt gta tat tat tcc gga gaa cat cct tcg caa tct tta ccg agc	576
Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu Pro Ser	
180 185 190	
gcg gga acg gtg aaa tat tcc ggc aac tgg caa tat atg acc gat gcc	624
Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala	

195	200	205	
ata cgt cat cga aca gga aaa gca gga gat cct agc gaa gat ttg ggt			672
Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp Leu Gly			
210	215	220	
tat atc gtt tat tac ggt caa aat gtc gga gca act tct tat gct gcg			720
Tyr Ile Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr Ala Ala			
225	230	235	240
act gcc gac gac cgg gag gga aaa cat cct gcc gaa tat acg gtt aat			768
Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr Val Asn			
	245	250	255
ttc gac caa aaa act ctg aat ggc aag ctg att aaa aat cag tat gtg			816
Phe Asp Gln Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr Val			
	260	265	270
caa aag aga gat gat cct aaa aaa cca ctg acc att tac gac att act			864
Gln Lys Arg Asp Asp Pro Lys Lys Pro Leu Thr Ile Tyr Asp Ile Thr			
	275	280	285
gca aaa ttg gac ggc aac cgc ttt acc ggc agt gcc aaa gtt aac aca			912
Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Thr			
	290	295	300
gag gtg aag acg aat cac gct gat aaa gaa tat ttg ttt ttc cat acc			960
Glu Val Lys Thr Asn His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr			
305	310	315	320
gat gcc gat cag cgg ctt gag ggc ggt ttt ttc ggc gat aag ggg gaa			1008
Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu			
	325	330	335
gag ctt gcc gga cgg ttt atc agc aac gac aac agc gta ttc ggc gtg			1056
Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val			
	340	345	350
ttc gca ggc aaa caa aaa aca gag aca gca aac gca tca gat aca aat			1104
Phe Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn			
	355	360	365
cct gcc ctg ccg tct gga aaa cac acc aaa atc ttg gat tct cta aaa			1152

Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys	
370	380
att tcc gtt gac gag gca agt ggt gaa aat ccc cga ccg ttt gag gtt	1200
Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Glu Val	
385	400
tcc act atg ccc gat ttt ggt cat ccc gac aaa ctt ctt gtc gaa ggg	1248
Ser Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly	
405	415
cgt gaa att cct ttg gta aac aaa gaa caa acc atc gat ctt gcc gac	1296
Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile Asp Leu Ala Asp	
420	430
ggc agg aaa atg acc gtc cgt gct tgt tgc gac ttt ttg acc tat gtg	1344
Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val	
435	445
aaa ctc gga cgg ata aaa acc gaa cgc ccc gcc gtc caa ccg aag gcg	1392
Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Gln Pro Lys Ala	
450	460
cag gat gaa gag ggg gac gaa gag ggt gta ggc gtt gat aac ggt aaa	1440
Gln Asp Glu Glu Gly Asp Glu Glu Gly Val Gly Val Asp Asn Gly Lys	
465	480
gaa agc gaa gac gaa atc ggc gat gaa gaa agc acc gga gac gaa gtc	1488
Glu Ser Glu Asp Glu Ile Gly Asp Glu Glu Ser Thr Gly Asp Glu Val	
485	495
gta gaa gat gaa gac gaa gat gaa gac gaa gaa gaa atc gaa gaa gaa	1536
Val Glu Asp Glu Asp Glu Asp Glu Asp Glu Glu Glu Ile Glu Glu Glu	
500	510
cct gaa gaa gaa gct gaa gag gaa gaa ccc gaa gaa gaa ttg ccg gca	1584
Pro Glu Glu Glu Ala Glu Glu Glu Glu Pro Glu Glu Glu Leu Pro Ala	
515	525
gaa gaa ggc aac ggc ggt tca ggc agc atc ctg ccc act ccg gaa gcc	1632
Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala	
530	540



tct aaa ggc agg gac atc gac ctt ttc ctg aaa ggt atc cgc acg gcg	1680
Ser Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala	
545                      550                      555                      560	
gaa gcc gac att cca aaa aac gga acg gcg cat tat acc ggc act tgg	1728
Glu Ala Asp Ile Pro Lys Asn Gly Thr Ala His Tyr Thr Gly Thr Trp	
565                      570                      575	
gaa gcg cgt atc ggc gta tcg gat agt ggt acg tcc att caa aag gat	1776
Glu Ala Arg Ile Gly Val Ser Asp Ser Gly Thr Ser Ile Gln Lys Asp	
580                      585                      590	
agc tat gcg aat caa ggg gca aaa gca gaa ttt acc gtt gat ttc gaa	1824
Ser Tyr Ala Asn Gln Gly Ala Lys Ala Glu Phe Thr Val Asp Phe Glu	
595                      600                      605	
gcg aag acg gtg tcc gga atg ctg aca gaa aaa aat gat aca acc ccc	1872
Ala Lys Thr Val Ser Gly Met Leu Thr Glu Lys Asn Asp Thr Thr Pro	
610                      615                      620	
gct ttt tat att gaa aaa ggt gtg att gac ggt aac ggt ttc cac gct	1920
Ala Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala	
625                      630                      635                      640	
ttg gcg cat act cgg gag aac ggt att gac ctt tct ggg cag ggt tcg	1968
Leu Ala His Thr Arg Glu Asn Gly Ile Asp Leu Ser Gly Gln Gly Ser	
645                      650                      655	
act aac ccg aag aac ttc aaa gcc gac aat ctt ctt gta aca ggc ggc	2016
Thr Asn Pro Lys Asn Phe Lys Ala Asp Asn Leu Leu Val Thr Gly Gly	
660                      665                      670	
ttt tat ggc ccg cag gcg gca gaa ttg ggc ggt aat att atc gac agc	2064
Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser	
675                      680                      685	
gac cgg aaa ttc ggt gcg gta ttt ggg gcg aaa aaa gat gac aag gag	2112
Asp Arg Lys Phe Gly Ala Val Phe Gly Ala Lys Lys Asp Asp Lys Glu	
690                      695                      700	
gca aca cga tga	2124
Ala Thr Arg	
705	

<210> 10  
 <211> 707  
 <212> PRT  
 <213> Neisseria meningitidis strain 881607

<400> 10  
 Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu  
 1 5 10 15  
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser  
 20 25 30  
 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr  
 35 40 45  
 Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Arg Pro  
 50 55 60  
 Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Ile Ala Thr Ser  
 65 70 75 80  
 Asp Lys Asp Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu Glu Lys  
 85 90 95  
 Leu Ser Phe Lys Glu Glu Asp Ile Leu Phe Leu Tyr Gly Ser Lys Lys  
 100 105 110  
 Asp Gln Arg Gln Gln Leu Lys Asp Lys Ile Arg Gln Pro Asn Pro Thr  
 115 120 125  
 Ala Ser Ile Thr Thr Ser Glu Lys Lys Asn Lys Lys Tyr Asp Tyr Lys  
 130 135 140  
 Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asp Gly Lys Asp Glu Ile  
 145 150 155 160  
 Glu Trp Thr Ser Asn Tyr Lys Gln Ser Thr Asn Arg Phe Gly Tyr Asp  
 165 170 175  
 Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu Pro Ser  
 180 185 190  
 Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala  
 195 200 205  
 Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp Leu Gly  
 210 215 220  
 Tyr Ile Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr Ala Ala  
 225 230 235 240  
 Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr Val Asn  
 245 250 255  
 Phe Asp Gln Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr Val  
 260 265 270  
 Gln Lys Arg Asp Asp Pro Lys Lys Pro Leu Thr Ile Tyr Asp Ile Thr

275	280	285
Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Thr		
290	295	300
Glu Val Lys Thr Asn His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr		
305	310	315
Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu		
325	330	335
Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val		
340	345	350
Phe Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn		
355	360	365
Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys		
370	375	380
Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Glu Val		
385	390	395
Ser Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly		
405	410	415
Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile Asp Leu Ala Asp		
420	425	430
Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val		
435	440	445
Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Gln Pro Lys Ala		
450	455	460
Gln Asp Glu Glu Gly Asp Glu Glu Gly Val Gly Val Asp Asn Gly Lys		
465	470	475
Glu Ser Glu Asp Glu Ile Gly Asp Glu Glu Ser Thr Gly Asp Glu Val		
485	490	495
Val Glu Asp Glu Asp Glu Asp Glu Asp Glu Glu Glu Ile Glu Glu Glu		
500	505	510
Pro Glu Glu Glu Ala Glu Glu Glu Glu Pro Glu Glu Glu Leu Pro Ala		
515	520	525
Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala		
530	535	540
Ser Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala		
545	550	555
Glu Ala Asp Ile Pro Lys Asn Gly Thr Ala His Tyr Thr Gly Thr Trp		
565	570	575
Glu Ala Arg Ile Gly Val Ser Asp Ser Gly Thr Ser Ile Gln Lys Asp		
580	585	590
Ser Tyr Ala Asn Gln Gly Ala Lys Ala Glu Phe Thr Val Asp Phe Glu		
595	600	605
Ala Lys Thr Val Ser Gly Met Leu Thr Glu Lys Asn Asp Thr Thr Pro		
610	615	620

Ala Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala  
625 630 635 640  
Leu Ala His Thr Arg Glu Asn Gly Ile Asp Leu Ser Gly Gln Gly Ser  
645 650 655  
Thr Asn Pro Lys Asn Phe Lys Ala Asp Asn Leu Leu Val Thr Gly Gly  
660 665 670  
Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser  
675 680 685  
Asp Arg Lys Phe Gly Ala Val Phe Gly Ala Lys Lys Asp Asp Lys Glu  
690 695 700  
Ala Thr Arg  
705

<210> 11  
<211> 94  
<212> DNA  
<213> Neisseria meningitidis

<400> 11  
cgggttgata ttatctgtac atattaatat aatgataatt attattaatc aaataggagg 60  
aaaagtaggg atgtgtaaac cgaattatgg cggc 94

<210> 12  
<211> 599  
<212> PRT  
<213> Neisseria meningitidis strain B16B6

<400> 12  
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
1 5 10 15  
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser  
20 25 30  
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu  
35 40 45  
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala  
50 55 60  
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn  
65 70 75 80  
Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys  
85 90 95  
Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu  
100 105 110

Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp  
 115 120 125  
 Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser  
 130 135 140  
 Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile  
 145 150 155 160  
 Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro  
 165 170 175  
 Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp  
 180 185 190  
 Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser  
 195 200 205  
 Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly  
 210 215 220  
 Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly  
 225 230 235 240  
 Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly  
 245 250 255  
 Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys  
 260 265 270  
 Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn  
 275 280 285  
 Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly  
 290 295 300  
 Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr  
 305 310 315 320  
 Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn  
 325 330 335  
 Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly  
 340 345 350  
 Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg  
 355 360 365  
 Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp  
 370 375 380  
 Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser  
 385 390 395 400  
 Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val  
 405 410 415  
 Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys  
 420 425 430  
 Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr  
 435 440 445  
 Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg

450		455		460	
Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu					
465		470		475	480
Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe					
	485		490		495
Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser					
	500		505		510
Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly					
	515		520		525
Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr					
	530		535		540
Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe					
545		550		555	560
Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly					
	565		570		575
Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala					
	580		585		590
Lys Arg Gln Gln Leu Val Gln					
595					